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## SEQUENCE LISTING

<110> Xiang, Rong  
 Zhou, He  
 Reisfeld, Ralph A.  
 The Scripps Research Institute

<120> DNA VACCINES AGAINST TUMOR GROWTH AND  
 METHODS OF USE THEREOF

<130> TSRI-874.1

<150> 60/457,009

<151> 2003-03-24

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<212> DNA

<213> HOMO SAPIENS

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Cys Thr Pro Glu Arg Met Ala Glu Ala Gly Phe Ile His Cys Pro Thr  
35 40 45  
Glu Asn Glu Pro Asp Leu Ala Gln Cys Phe Phe Cys Phe Lys Glu Leu  
50 55 60  
Glu Gly Trp Glu Pro Asp Asp Asp Pro Ile Glu Glu His Lys Lys His  
65 70 75 80  
Ser Ser Gly Cys Ala Phe Leu Ser Val Lys Lys Gln Phe Glu Glu Leu  
85 90 95  
Thr Leu Gly Glu Phe Leu Lys Leu Asp Arg Glu Arg Ala Lys Asn Lys  
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Cys Thr Pro Glu Arg Met Ala Glu Ala Gly Phe Ile His Cys Pro Thr
          35           40           45
Glu Asn Glu Pro Asp Leu Ala Gln Cys Phe Phe Cys Phe Lys Glu Leu
          50           55           60
Glu Gly Trp Glu Pro Asp Asp Asn Pro Ile Glu Glu His Arg Lys His
65           70           75           80
Ser Pro Gly Cys Ala Phe Leu Thr Val Lys Lys Gln Met Glu Glu Leu
          85           90           95
Thr Val Ser Glu Phe Leu Lys Leu Asp Arg Gln Arg Ala Lys Asn Lys
          100          105          110
Ile Ala Lys Glu Thr Asn Asn Lys Gln Lys Glu Phe Glu Glu Thr Ala
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<210> 5

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<212> DNA

<213> HOMO SAPIENS

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gcaggactgt ccccttgaag gagaatcatc aggacctgg acctgatacg gctccccagt 780
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<213> HOMO SAPIENS

<400> 6

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			20					25					30					
Leu	Lys	Tyr	Ser	Gln	Arg	Lys	Ile	Pro	Ala	Lys	Val	Val	Arg	Ser	Tyr			
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Arg	Lys	Gln	Glu	Pro	Ser	Leu	Gly	Cys	Ser	Ile	Pro	Ala	Ile	Leu	Phe			
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Leu	Pro	Arg	Lys	Arg	Ser	Gln	Ala	Glu	Leu	Cys	Ala	Asp	Pro	Lys	Glu			
65					70					75					80			
Leu	Trp	Val	Gln	Gln	Leu	Met	Gln	His	Leu	Asp	Lys	Thr	Pro	Ser	Pro			
			85					90					95					
Gln	Lys	Pro	Ala	Gln	Gly	Cys	Arg	Lys	Asp	Arg	Gly	Ala	Ser	Lys	Thr			
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Gly	Lys	Lys	Gly	Lys	Gly	Ser	Lys	Gly	Cys	Lys	Arg	Thr	Glu	Arg	Ser			
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		20						25				30						
Leu	Lys	Tyr	Ser	Gln	Lys	Lys	Ile	Pro	Tyr	Ser	Ile	Val	Arg	Gly	Tyr			
		35					40					45						
Arg	Lys	Gln	Glu	Pro	Ser	Leu	Gly	Cys	Pro	Ile	Pro	Ala	Ile	Leu	Phe			
	50					55					60							
Ser	Pro	Arg	Lys	His	Ser	Lys	Pro	Glu	Leu	Cys	Ala	Asn	Pro	Glu	Glu			
65					70					75					80			

Gly Trp Val Gln Asn Leu Met Arg Arg Leu Asp Gln Pro Pro Ala Pro  
85 90 95  
Gly Lys Gln Ser Pro Gly Cys Arg Lys Asn Arg Gly Thr Ser Lys Ser  
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Asp Ser Leu Ser Cys Glu Leu Thr Phe Asn Tyr Arg Asn Leu His Gly  
35 40 45  
Gln Cys Ser Val Asn Gly Lys Thr Leu Leu Asp Phe Gly Asp Lys Lys  
50 55 60  
His Glu Glu Asn Ala Thr Lys Met Cys Ala Asp Leu Ser Gln Asn Leu  
65 70 75 80  
Arg Glu Ile Ser Glu Glu Met Trp Lys Leu Gln Ser Gly Asn Asp Thr  
85 90 95  
Leu Asn Val Thr Thr Gln Ser Gln Tyr Asn Gln Gly Lys Phe Ile Asp  
100 105 110  
Gly Phe Trp Ala Ile Asn Thr Asp Glu Gln His Ser Ile Tyr Phe Tyr  
115 120 125  
Pro Leu Asn Met Thr Trp Arg Glu Ser His Ser Asp Asn Ser Ser Ala

130		135		140
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Leu Ile Thr Tyr Phe Ser His Cys Leu Asn Lys Ser Ser Ser His Phe				
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Arg Glu Met Pro Lys Ser Thr Leu Lys Val Pro Asp Thr Thr Gln Arg				
	180		185	190
Thr Asn Ala Thr Gln Ile His Pro Thr Val Asn Asn Phe Arg His Asn				
	195		200	205
Ser Asp Asn Gln Gly Leu Ser Val Thr Trp Ile Val Ile Ile Cys Ile				
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Leu Lys Lys Lys				240

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35 40 45  
Arg Lys Gln Glu Pro Ser Leu Gly Cys Ser Ile Pro Ala Ile Leu Phe  
50 55 60

Leu Pro Arg Lys Arg Ser Gln Ala Glu Leu Cys Ala Asp Pro Lys Glu  
65 70 75 80  
Leu Trp Val Gln Gln Leu Met Gln His Leu Asp Lys Thr Pro Ser Pro  
85 90 95  
Gln Lys Pro Ala Gln Gly Cys Arg Lys Asp Arg Gly Ala Ser Lys Thr  
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Thr Val Leu Ser Trp Asp Gly Ser Val Gln Ser Gly Phe Leu Thr Glu  
35 40 45  
Val His Leu Asp Gly Gln Pro Phe Leu Arg Cys Asp Arg Gln Lys Cys  
50 55 60

Arg	Ala	Lys	Pro	Gln	Gly	Gln	Trp	Ala	Glu	Asp	Val	Leu	Gly	Asn	Lys	65	70	75	80
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Ser	Ser	Gln	His	Phe	Tyr	Tyr	Asp	Gly	Glu	Leu	Phe	Leu	Ser	Gln	Asn	130	135	140	
Leu	Glu	Thr	Lys	Glu	Trp	Thr	Met	Pro	Gln	Ser	Ser	Arg	Ala	Gln	Thr	145	150	155	160
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Lys	Thr	His	Tyr	His	Ala	Met	His	Ala	Asp	Cys	Leu	Gln	Glu	Leu	Arg	180	185	190	
Arg	Tyr	Leu	Lys	Ser	Gly	Val	Val	Leu	Arg	Arg	Thr	Val	Pro	Pro	Met	195	200	205	
Val	Asn	Val	Thr	Arg	Ser	Glu	Ala	Ser	Glu	Gly	Asn	Ile	Thr	Val	Thr	210	215	220	
Cys	Arg	Ala	Ser	Gly	Phe	Tyr	Pro	Trp	Asn	Ile	Thr	Leu	Ser	Trp	Arg	225	230	235	240
Gln	Asp	Gly	Val	Ser	Leu	Ser	His	Asp	Thr	Gln	Gln	Trp	Gly	Asp	Val	245	250	255	
Leu	Pro	Asp	Gly	Asn	Gly	Thr	Tyr	Gln	Thr	Trp	Val	Ala	Thr	Arg	Ile	260	265	270	
Cys	Gln	Gly	Glu	Glu	Gln	Arg	Phe	Thr	Cys	Tyr	Met	Glu	His	Ser	Gly	275	280	285	
Asn	His	Ser	Thr	His	Pro	Val	Pro	Ser	Gly	Lys	Val	Leu	Val	Leu	Gln	290	295	300	
Ser	His	Trp	Gln	Thr	Phe	His	Val	Ser	Ala	Val	Ala	Ala	Ala	Ala	Ala	305	310	315	320
Ile	Phe	Val	Ile	Ile	Ile	Phe	Tyr	Val	Arg	Cys	Cys	Lys	Lys	Lys	Thr	325	330	335	
Ser	Ala	Ala	Glu	Gly	Pro	Glu	Leu	Val	Ser	Leu	Gln	Val	Leu	Asp	Gln	340	345	350	
His	Pro	Val	Gly	Thr	Ser	Asp	His	Arg	Asp	Ala	Thr	Gln	Leu	Gly	Phe	355	360	365	
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<212> DNA

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atgacaggca gaaacgcagg gcaaagcccc agggacagtg ggcagaagat gtcctgggag 240
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<210> 16

<211> 383

<212> PRT

<213> HOMO SAPIENS

<400> 16

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Ala Pro Pro Ala Ala Ala Ala Glu Pro His Ser Leu Arg Tyr Asn Leu
          20           25           30
Met Val Leu Ser Gln Asp Gly Ser Val Gln Ser Gly Phe Leu Ala Glu
          35           40           45
Gly His Leu Asp Gly Gln Pro Phe Leu Arg Tyr Asp Arg Gln Lys Arg
          50           55           60
Arg Ala Lys Pro Gln Gly Gln Trp Ala Glu Asp Val Leu Gly Ala Glu
65           70           75           80
Thr Trp Asp Thr Glu Thr Glu Asp Leu Thr Glu Asn Gly Gln Asp Leu

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				85					90					95			
Arg	Arg	Thr	Leu	Thr	His	Ile	Lys	Asp	Gln	Lys	Gly	Gly	Leu	His	Ser		
			100					105					110				
Leu	Gln	Glu	Ile	Arg	Val	Cys	Glu	Ile	His	Glu	Asp	Ser	Ser	Thr	Arg		
			115				120					125					
Gly	Ser	Arg	His	Phe	Tyr	Tyr	Asn	Gly	Glu	Leu	Phe	Leu	Ser	Gln	Asn		
			130			135					140						
Leu	Glu	Thr	Gln	Glu	Ser	Thr	Val	Pro	Gln	Ser	Ser	Arg	Ala	Gln	Thr		
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Leu	Ala	Met	Asn	Val	Thr	Asn	Phe	Trp	Lys	Glu	Asp	Ala	Met	Lys	Thr		
			165					170						175			
Lys	Thr	His	Tyr	Arg	Ala	Met	Gln	Ala	Asp	Cys	Leu	Gln	Lys	Leu	Gln		
			180					185					190				
Arg	Tyr	Leu	Lys	Ser	Gly	Val	Ala	Ile	Arg	Arg	Thr	Val	Pro	Pro	Met		
			195				200					205					
Val	Asn	Val	Thr	Cys	Ser	Glu	Val	Ser	Glu	Gly	Asn	Ile	Thr	Val	Thr		
			210			215					220						
Cys	Arg	Ala	Ser	Ser	Phe	Tyr	Pro	Arg	Asn	Ile	Thr	Leu	Thr	Trp	Arg		
225					230				235						240		
Gln	Asp	Gly	Val	Ser	Leu	Ser	His	Asn	Thr	Gln	Gln	Trp	Gly	Asp	Val		
			245					250						255			
Leu	Pro	Asp	Gly	Asn	Gly	Thr	Tyr	Gln	Thr	Trp	Val	Ala	Thr	Arg	Ile		
			260					265					270				
Arg	Gln	Gly	Glu	Glu	Gln	Arg	Phe	Thr	Cys	Tyr	Met	Glu	His	Ser	Gly		
			275				280					285					
Asn	His	Gly	Thr	His	Pro	Val	Pro	Ser	Gly	Lys	Ala	Leu	Val	Leu	Gln		
			290			295					300						
Ser	Gln	Arg	Thr	Asp	Phe	Pro	Tyr	Val	Ser	Ala	Ala	Met	Pro	Cys	Phe		
305					310					315					320		
Val	Ile	Ile	Ile	Ile	Leu	Cys	Val	Pro	Cys	Cys	Lys	Lys	Lys	Thr	Ser		
			325					330						335			
Ala	Ala	Glu	Gly	Pro	Glu	Leu	Val	Ser	Leu	Gln	Val	Leu	Asp	Gln	His		
			340					345					350				
Pro	Val	Gly	Thr	Gly	Asp	His	Arg	Asp	Ala	Ala	Gln	Leu	Gly	Phe	Gln		
		355				360					365						
Pro	Leu	Met	Ser	Ala	Thr	Gly	Ser	Thr	Gly	Ser	Thr	Glu	Gly	Ala			
		370				375					380						

<210> 17

<211> 735

<212> DNA

<213> HOMO SAPIENS

<400> 17

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cctaagtcca gacctgaacc acagtgggtg gaagttcaag gcctgggtga tgaaaggcct 180
tttcttcact atgactgtgt taaccacaag gccaaagcct ttgcttctct ggggaagaaa 240
gtcaatgtca caaaaacctg ggaagaacaa actgaaacac taagagacgt ggtggatttc 300
cttaaagggc aactgcttga cattcaagtg gagaatttaa taccattga gccctcacc 360
ctgcaggcca ggatgtcttg tgagcatgaa gccatggac acggcagagg atcttggcag 420
ttcctcttca atggacagaa gttcctctc tttgactcaa acaacagaaa gtggacagca 480

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cttcacccctg gagccaagaa gatgacagag aagtgggaga agaacaggga tgtgaccatg 540  
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tggaacaaa tgctggatcc aacaaaacca ccctctctgg cccagggcac aacccaaccc 660  
aaggccatgg ccaccaccct cagtccttgg agccttctca tcattcttct ctgcttcatt 720  
ctagctggca gatga 735

<210> 18  
<211> 244  
<212> PRT  
<213> HOMO SAPIENS

<400> 18  
Met Ala Ala Ala Ala Ser Pro Ala Phe Leu Leu Cys Leu Pro Leu Leu  
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His Leu Leu Ser Gly Trp Ser Arg Ala Gly Trp Val Asp Thr His Cys  
20 25 30  
Leu Cys Tyr Asp Phe Ile Ile Thr Pro Lys Ser Arg Pro Glu Pro Gln  
35 40 45  
Trp Cys Glu Val Gln Gly Leu Val Asp Glu Arg Pro Phe Leu His Tyr  
50 55 60  
Asp Cys Val Asn His Lys Ala Lys Ala Phe Ala Ser Leu Gly Lys Lys  
65 70 75 80  
Val Asn Val Thr Lys Thr Trp Glu Glu Gln Thr Glu Thr Leu Arg Asp  
85 90 95  
Val Val Asp Phe Leu Lys Gly Gln Leu Leu Asp Ile Gln Val Glu Asn  
100 105 110  
Leu Ile Pro Ile Glu Pro Leu Thr Leu Gln Ala Arg Met Ser Cys Glu  
115 120 125  
His Glu Ala His Gly His Gly Arg Gly Ser Trp Gln Phe Leu Phe Asn  
130 135 140  
Gly Gln Lys Phe Leu Leu Phe Asp Ser Asn Asn Arg Lys Trp Thr Ala  
145 150 155 160  
Leu His Pro Gly Ala Lys Lys Met Thr Glu Lys Trp Glu Lys Asn Arg  
165 170 175  
Asp Val Thr Met Phe Phe Gln Lys Ile Ser Leu Gly Asp Cys Lys Met  
180 185 190  
Trp Leu Glu Glu Phe Leu Met Tyr Trp Glu Gln Met Leu Asp Pro Thr  
195 200 205  
Lys Pro Pro Ser Leu Ala Pro Gly Thr Thr Gln Pro Lys Ala Met Ala  
210 215 220  
Thr Thr Leu Ser Pro Trp Ser Leu Leu Ile Ile Phe Leu Cys Phe Ile  
225 230 235 240  
Leu Ala Gly Arg

<210> 19  
<211> 741  
<212> DNA  
<213> HOMO SAPIENS

<400> 19  
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cctaagtcca gacctggacc acggtggtgt gcggttcaag gccaggtgga tgaaaagact 180
tttcttcact atgactgtgg caacaagaca gtcacacctg tcagtcccct ggggaagaaa 240
ctaaatgtca caacggcctg gaaagcacag aaccaggtac tgagagaggt ggtggacata 300
cttacagagc aactgctga cattcagctg gagaattaca cacccaagga acccctcacc 360
ctgcaggcaa ggatgtcttg tgagcagaaa gctgaaggac acagcagtgg atcttggcag 420
ttcagtttcg atgggcagat cttcctctc tttgactcag agaagagaat gtggacaacg 480
gttcacacctg gagccagaaa gatgaaagaa aagtgggaga atgacaaggt tgtggccatg 540
tccttccatt acttctcaat gggagactgt ataggatggc ttgaggactt cttgatgggc 600
atggacagca ccctggagcc aagtgcagga gcaccactcg ccatgtctc aggcacaacc 660
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ttcatcctcc ctggcatctg a                                     741

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<210> 20

<211> 246

<212> PRT

<213> HOMO SAPIENS

<400> 20

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 20          25          30
Leu Cys Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg Pro Gly Pro Arg
 35          40          45
Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr Phe Leu His Tyr
 50          55          60
Asp Cys Gly Asn Lys Thr Val Thr Pro Val Ser Pro Leu Gly Lys Lys
 65          70          75          80
Leu Asn Val Thr Thr Ala Trp Lys Ala Gln Asn Pro Val Leu Arg Glu
 85          90          95
Val Val Asp Ile Leu Thr Glu Gln Leu Arg Asp Ile Gln Leu Glu Asn
100         105         110
Tyr Thr Pro Lys Glu Pro Leu Thr Leu Gln Ala Arg Met Ser Cys Glu
115         120         125
Gln Lys Ala Glu Gly His Ser Ser Gly Ser Trp Gln Phe Ser Phe Asp
130         135         140
Gly Gln Ile Phe Leu Leu Phe Asp Ser Glu Lys Arg Met Trp Thr Thr
145         150         155         160
Val His Pro Gly Ala Arg Lys Met Lys Glu Lys Trp Glu Asn Asp Lys
165         170         175
Val Val Ala Met Ser Phe His Tyr Phe Ser Met Gly Asp Cys Ile Gly
180         185         190
Trp Leu Glu Asp Phe Leu Met Gly Met Asp Ser Thr Leu Glu Pro Ser
195         200         205
Ala Gly Ala Pro Leu Ala Met Ser Ser Gly Thr Thr Gln Leu Arg Ala
210         215         220
Thr Ala Thr Thr Leu Ile Leu Cys Cys Leu Leu Ile Ile Leu Pro Cys
225         230         235         240
Phe Ile Leu Pro Gly Ile
245

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<210> 21  
 <211> 735  
 <212> DNA  
 <213> HOMO SAPIENS

<400> 21  
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 attcatttgc ccagacatgg gcaacagtgg tgtgaggtcc agagccaggt ggatcagaag 180  
 aattttctct cctatgactg tggcagtgc aaggtcttat ctatgggtca cctagaagag 240  
 cagctgtatg ccacagatgc ctggggaaaa caactggaaa tgctgagaga ggtggggcag 300  
 aggtcagac tgggaactggc tgacactgag ctggaggatt tcacaccag tggaccctc 360  
 acgctgcagg tcaggatgtc ttgtgagtgt gaagccgatg gatacatccg tggatcttgg 420  
 cagttcagct tcgatggacg gaagttcctc ctctttgact caaacaacag aaagtggaca 480  
 gtggttcacg ctggagccag gcggatgaaa gagaagtggg agaaggatag cggactgacc 540  
 accttcttca agatggtctc aatgagagac tgcaagagct ggcttaggga cttcctgatg 600  
 cacaggaaga agaggctgga acccacagca ccaccacca tggccccagg cttagctcaa 660  
 cccaaagcca tagccaccac cctcagtcctc tggagcttcc tcatcatcct ctgcttcac 720  
 ctccctggca tctga 735

<210> 22  
 <211> 244  
 <212> PRT  
 <213> HOMO SAPIENS

<400> 22  
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 Pro Tyr Leu Leu Phe Asp Trp Ser Gly Thr Gly Arg Ala Asp Ala His  
 20 25 30  
 Ser Leu Trp Tyr Asn Phe Thr Ile His Leu Pro Arg His Gly Gln  
 35 40 45  
 Gln Trp Cys Glu Val Gln Ser Gln Val Asp Gln Lys Asn Phe Leu Ser  
 50 55 60  
 Tyr Asp Cys Gly Ser Asp Lys Val Leu Ser Met Gly His Leu Glu Glu  
 65 70 75 80  
 Gln Leu Tyr Ala Thr Asp Ala Trp Gly Lys Gln Leu Glu Met Leu Arg  
 85 90 95  
 Glu Val Gly Gln Arg Leu Arg Leu Glu Leu Ala Asp Thr Glu Leu Glu  
 100 105 110  
 Asp Phe Thr Pro Ser Gly Pro Leu Thr Leu Gln Val Arg Met Ser Cys  
 115 120 125  
 Glu Cys Glu Ala Asp Gly Tyr Ile Arg Gly Ser Trp Gln Phe Ser Phe  
 130 135 140  
 Asp Gly Arg Lys Phe Leu Leu Phe Asp Ser Asn Asn Arg Lys Trp Thr  
 145 150 155 160  
 Val Val His Ala Gly Ala Arg Arg Met Lys Glu Lys Trp Glu Lys Asp  
 165 170 175  
 Ser Gly Leu Thr Thr Phe Phe Lys Met Val Ser Met Arg Asp Cys Lys  
 180 185 190  
 Ser Trp Leu Arg Asp Phe Leu Met His Arg Lys Lys Arg Leu Glu Pro  
 195 200 205  
 Thr Ala Pro Pro Thr Met Ala Pro Gly Leu Ala Gln Pro Lys Ala Ile

210	215	220
Ala Thr Thr Leu Ser Pro Trp Ser Phe Leu Ile Ile Leu Cys Phe Ile		
225	230	235
Leu Pro Gly Ile		240

<210> 23  
<211> 165  
<212> PRT  
<213> HOMO SAPIENS

<400> 23  
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His Arg Ile Ser Thr Phe Lys Asn Trp Pro Phe Leu Glu Gly Cys Ala  
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Cys Thr Pro Glu Arg Met Ala Glu Ala Gly Phe Ile His Cys Pro Thr  
35 40 45  
Glu Asn Glu Pro Asp Leu Ala Gln Cys Phe Phe Cys Phe Lys Glu Leu  
50 55 60  
Glu Gly Trp Glu Pro Asp Asp Asp Pro Ile Gly Pro Gly Thr Val Ala  
65 70 75 80  
Tyr Ala Cys Asn Thr Ser Thr Leu Gly Gly Arg Gly Gly Arg Ile Thr  
85 90 95  
Arg Glu Glu His Lys Lys His Ser Ser Gly Cys Ala Phe Leu Ser Val  
100 105 110  
Lys Lys Gln Phe Glu Glu Leu Thr Leu Gly Glu Phe Leu Lys Leu Asp  
115 120 125  
Arg Glu Arg Ala Lys Asn Lys Ile Ala Lys Glu Thr Asn Asn Lys Lys  
130 135 140  
Lys Glu Phe Glu Glu Thr Ala Lys Lys Val Arg Arg Ala Ile Glu Gln  
145 150 155 160  
Leu Ala Ala Met Asp  
165

<210> 24  
<211> 137  
<212> PRT  
<213> HOMO SAPIENS

<400> 24  
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His Arg Ile Ser Thr Phe Lys Asn Trp Pro Phe Leu Glu Gly Cys Ala  
20 25 30  
Cys Thr Pro Glu Arg Met Ala Glu Ala Gly Phe Ile His Cys Pro Thr  
35 40 45  
Glu Asn Glu Pro Asp Leu Ala Gln Cys Phe Phe Cys Phe Lys Glu Leu  
50 55 60  
Glu Gly Trp Glu Pro Asp Asp Asp Pro Met Gln Arg Lys Pro Thr Ile  
65 70 75 80

Arg	Arg	Lys	Asn	Leu	Arg	Lys	Leu	Arg	Arg	Lys	Cys	Ala	Val	Pro	Ser
				85					90					95	
Ser	Ser	Trp	Leu	Pro	Trp	Ile	Glu	Ala	Ser	Gly	Arg	Ser	Cys	Leu	Val
			100					105					110		
Pro	Glu	Trp	Leu	His	His	Phe	Gln	Gly	Leu	Phe	Pro	Gly	Ala	Thr	Ser
			115				120					125			
Leu	Pro	Val	Gly	Pro	Leu	Ala	Met	Ser							
		130				135									

<210> 25  
 <211> 9  
 <212> PRT  
 <213> HOMO SAPIENS

<400> 25  
 Ala Tyr Ala Cys Asn Thr Ser Thr Leu  
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<210> 26  
 <211> 1322  
 <212> DNA  
 <213> homo sapiens

<220>  
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 ggccatcagc ccccatcttct gctgcaaacc tggtcagagc cagtgttccc tcc atg 176  
 Met  
 1

gga	cct	aaa	gac	agt	gcc	aag	tgc	ctg	cac	cgt	gga	cca	cag	ccg	agc	224
Gly	Pro	Lys	Asp	Ser	Ala	Lys	Cys	Leu	His	Arg	Gly	Pro	Gln	Pro	Ser	
		5						10					15			

cac	tgg	gca	gcc	ggg	gat	ggg	ccc	acg	cag	gag	cgc	tgt	gga	ccc	cgc	272
His	Trp	Ala	Ala	Gly	Asp	Gly	Pro	Thr	Gln	Glu	Arg	Cys	Gly	Pro	Arg	
		20					25					30				

tct	ctg	ggc	agc	cct	gtc	cta	ggc	ctg	gac	acc	tgc	aga	gcc	tgg	gac	320
Ser	Leu	Gly	Ser	Pro	Val	Leu	Gly	Leu	Asp	Thr	Cys	Arg	Ala	Trp	Asp	
		35					40				45					

cac	gtg	gat	ggg	cag	atc	ctg	ggc	cag	ctg	cgg	ccc	ctg	aca	gag	gag	368
His	Val	Asp	Gly	Gln	Ile	Leu	Gly	Gln	Leu	Arg	Pro	Leu	Thr	Glu	Glu	
		50				55				60					65	

gaa	gag	gag	gag	ggc	gcc	ggg	gcc	acc	ttg	tcc	agg	ggg	cct	gcc	ttc	416
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Glu	Glu	Glu	Glu	Gly	Ala	Gly	Ala	Thr	Leu	Ser	Arg	Gly	Pro	Ala	Phe	
				70					75					80		
ccc	ggc	atg	ggc	tct	gag	gag	ttg	cgt	ctg	gcc	tcc	ttc	tat	gac	tgg	464
Pro	Gly	Met	Gly	Ser	Glu	Glu	Leu	Arg	Leu	Ala	Ser	Phe	Tyr	Asp	Trp	
			85					90				95				
ccg	ctg	act	gct	gag	gtg	cca	ccc	gag	ctg	ctg	gct	gct	gcc	ggc	ttc	512
Pro	Leu	Thr	Ala	Glu	Val	Pro	Pro	Glu	Leu	Leu	Ala	Ala	Ala	Gly	Phe	
		100					105					110				
ttc	cac	aca	ggc	cat	cag	gac	aag	gtg	agg	tgc	ttc	ttc	tgc	tat	ggg	560
Phe	His	Thr	Gly	His	Gln	Asp	Lys	Val	Arg	Cys	Phe	Phe	Cys	Tyr	Gly	
	115					120				125						
ggc	ctg	cag	agc	tgg	aag	cgc	ggg	gac	gac	ccc	tgg	acg	gag	cat	gcc	608
Gly	Leu	Gln	Ser	Trp	Lys	Arg	Gly	Asp	Asp	Pro	Trp	Thr	Glu	His	Ala	
130					135					140					145	
aag	tgg	ttc	ccc	agc	tgt	cag	ttc	ctg	ctc	cgg	tca	aaa	gga	aga	gac	656
Lys	Trp	Phe	Pro	Ser	Cys	Gln	Phe	Leu	Leu	Arg	Ser	Lys	Gly	Arg	Asp	
			150					155					160			
ttt	gtc	cac	agt	gtg	cag	gag	act	cac	tcc	cag	ctg	ctg	ggc	tcc	tgg	704
Phe	Val	His	Ser	Val	Gln	Glu	Thr	His	Ser	Gln	Leu	Leu	Gly	Ser	Trp	
		165						170					175			
gac	ccg	tgg	gaa	gaa	ccg	gaa	gac	gca	gcc	cct	gtg	gcc	ccc	tcc	gtc	752
Asp	Pro	Trp	Glu	Glu	Pro	Glu	Asp	Ala	Ala	Pro	Val	Ala	Pro	Ser	Val	
		180					185					190				
cct	gcc	tct	ggg	tac	cct	gag	ctg	ccc	aca	ccc	agg	aga	gag	gtc	cag	800
Pro	Ala	Ser	Gly	Tyr	Pro	Glu	Leu	Pro	Thr	Pro	Arg	Arg	Glu	Val	Gln	
		195				200					205					
tct	gaa	agt	gcc	cag	gag	cca	gga	ggg	gtc	agt	cca	gcc	gag	gcc	cag	848
Ser	Glu	Ser	Ala	Gln	Glu	Pro	Gly	Gly	Val	Ser	Pro	Ala	Glu	Ala	Gln	
210					215				220					225		
agg	gcg	tgg	tgg	gtt	ctt	gag	ccc	cca	gga	gcc	agg	gat	gtg	gag	gcg	896
Arg	Ala	Trp	Trp	Val	Leu	Glu	Pro	Pro	Gly	Ala	Arg	Asp	Val	Glu	Ala	
				230					235				240			
cag	ctg	cgg	cgg	ctg	cag	gag	gag	agg	acg	tgc	aag	gtg	tgc	ctg	gac	944
Gln	Leu	Arg	Arg	Leu	Gln	Glu	Glu	Arg	Thr	Cys	Lys	Val	Cys	Leu	Asp	
			245					250					255			
cgc	gcc	gtg	tcc	atc	gtc	ttt	gtg	ccg	tgc	ggc	cac	ctg	gtc	tgt	gct	992
Arg	Ala	Val	Ser	Ile	Val	Phe	Val	Pro	Cys	Gly	His	Leu	Val	Cys	Ala	
		260					265					270				
gag	tgt	gcc	ccc	ggc	ctg	cag	ctg	tgc	ccc	atc	tgc	aga	gcc	ccc	gtc	1040
Glu	Cys	Ala	Pro	Gly	Leu	Gln	Leu	Cys	Pro	Ile	Cys	Arg	Ala	Pro	Val	



275 280 285

cgc agc cgc gtg cgc acc ttc ctg tcc tag gccaggtgcc atggccggcc 1090  
 Arg Ser Arg Val Arg Thr Phe Leu Ser \*  
 290 295

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 35 40 45  
 Asp His Val Asp Gly Gln Ile Leu Gly Gln Leu Arg Pro Leu Thr Glu  
 50 55 60  
 Glu Glu Glu Glu Glu Gly Ala Gly Ala Thr Leu Ser Arg Gly Pro Ala  
 65 70 75 80  
 Phe Pro Gly Met Gly Ser Glu Glu Leu Arg Leu Ala Ser Phe Tyr Asp  
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 Trp Pro Leu Thr Ala Glu Val Pro Pro Glu Leu Leu Ala Ala Ala Gly  
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 Phe Phe His Thr Gly His Gln Asp Lys Val Arg Cys Phe Phe Cys Tyr  
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 Gly Gly Leu Gln Ser Trp Lys Arg Gly Asp Asp Pro Trp Thr Glu His  
 130 135 140  
 Ala Lys Trp Phe Pro Ser Cys Gln Phe Leu Leu Arg Ser Lys Gly Arg  
 145 150 155 160  
 Asp Phe Val His Ser Val Gln Glu Thr His Ser Gln Leu Leu Gly Ser  
 165 170 175  
 Trp Asp Pro Trp Glu Glu Pro Glu Asp Ala Ala Pro Val Ala Pro Ser  
 180 185 190  
 Val Pro Ala Ser Gly Tyr Pro Glu Leu Pro Thr Pro Arg Arg Glu Val  
 195 200 205  
 Gln Ser Glu Ser Ala Gln Glu Pro Gly Gly Val Ser Pro Ala Glu Ala  
 210 215 220  
 Gln Arg Ala Trp Trp Val Leu Glu Pro Pro Gly Ala Arg Asp Val Glu  
 225 230 235 240  
 Ala Gln Leu Arg Arg Leu Gln Glu Glu Arg Thr Cys Lys Val Cys Leu  
 245 250 255  
 Asp Arg Ala Val Ser Ile Val Phe Val Pro Cys Gly His Leu Val Cys  
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 Ala Glu Cys Ala Pro Gly Leu Gln Leu Cys Pro Ile Cys Arg Ala Pro  
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Val Arg Ser Arg Val Arg Thr Phe Leu Ser  
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ggccatcagc ccccatcttct gctgcaaacc tggtcagagc cagtgttccc tcc atg 176  
Met  
1

gga cct aaa gac agt gcc aag tgc ctg cac cgt gga cca cag ccg agc 224  
Gly Pro Lys Asp Ser Ala Lys Cys Leu His Arg Gly Pro Gln Pro Ser  
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cac tgg gca gcc ggt gat ggt ccc acg cag gag cgc tgt gga ccc cgc 272  
His Trp Ala Ala Gly Asp Gly Pro Thr Gln Glu Arg Cys Gly Pro Arg  
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tct ctg ggc agc cct gtc cta ggc ctg gac acc tgc aga gcc tgg gac 320  
Ser Leu Gly Ser Pro Val Leu Gly Leu Asp Thr Cys Arg Ala Trp Asp  
35 40 45

cac gtg gat ggg cag atc ctg ggc cag ctg cgg ccc ctg aca gag gag 368  
His Val Asp Gly Gln Ile Leu Gly Gln Leu Arg Pro Leu Thr Glu Glu  
50 55 60 65

gaa gag gag gag ggc gcc ggg gcc acc ttg tcc agg ggg cct gcc ttc 416  
Glu Glu Glu Glu Gly Ala Gly Ala Thr Leu Ser Arg Gly Pro Ala Phe  
70 75 80

ccc ggc atg ggc tct gag gag ttg cgt ctg gcc tcc ttc tat gac tgg 464  
Pro Gly Met Gly Ser Glu Glu Leu Arg Leu Ala Ser Phe Tyr Asp Trp  
85 90 95

ccg ctg act gct gag gtg cca ccc gag ctg ctg gct gct gcc ggc ttc 512  
Pro Leu Thr Ala Glu Val Pro Pro Glu Leu Leu Ala Ala Ala Gly Phe  
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ttc cac aca ggc cat cag gac aag gtg agg tgc ttc ttc tgc tat ggg 560  
Phe His Thr Gly His Gln Asp Lys Val Arg Cys Phe Phe Cys Tyr Gly  
115 120 125

ggc ctg cag agc tgg aag cgc ggg gac gac ccc tgg acg gag cat gcc 608

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Lys	Trp	Phe	Pro	Ser	Cys	Gln	Phe	Leu	Leu	Arg	Ser	Lys	Gly	Arg	Asp		
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Phe	Val	His	Ser	Val	Gln	Glu	Thr	His	Ser	Gln	Leu	Leu	Gly	Ser	Trp		
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gac	ccg	tgg	gaa	gaa	ccg	gaa	gac	gca	gcc	cct	gtg	gcc	ccc	tcc	gtc	752	
Asp	Pro	Trp	Glu	Glu	Pro	Glu	Asp	Ala	Ala	Pro	Val	Ala	Pro	Ser	Val		
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Pro	Ala	Ser	Gly	Tyr	Pro	Glu	Leu	Pro	Thr	Pro	Arg	Arg	Glu	Val	Gln		
	195				200					205							
tct	gaa	agt	gcc	cag	gag	cca	gga	gcc	agg	gat	gtg	gag	gcg	cag	ctg	848	
Ser	Glu	Ser	Ala	Gln	Glu	Pro	Gly	Ala	Arg	Asp	Val	Glu	Ala	Gln	Leu		
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Arg	Arg	Leu	Gln	Glu	Glu	Arg	Thr	Cys	Lys	Val	Cys	Leu	Asp	Arg	Ala		
			230					235					240				
gtg	tcc	atc	gtc	ttt	gtg	ccg	tgc	ggc	cac	ctg	gtc	tgt	gct	gag	tgt	944	
Val	Ser	Ile	Val	Phe	Val	Pro	Cys	Gly	His	Leu	Val	Cys	Ala	Glu	Cys		
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gcc	ccc	ggc	ctg	cag	ctg	tgc	ccc	atc	tgc	aga	gcc	ccc	gtc	cgc	agc	992	
Ala	Pro	Gly	Leu	Gln	Leu	Cys	Pro	Ile	Cys	Arg	Ala	Pro	Val	Arg	Ser		
		260				265					270						
cgc	gtg	cgc	acc	ttc	ctg	tcc	tag	gccaggtgcc	atggccggcc	aggtgggctg	1046						
Arg	Val	Arg	Thr	Phe	Leu	Ser	*										
	275				280												
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